012679-093.ST25

SEQUENCE LISTING

<110> Kim, Sunghoon

<120> Method for Stimulating Wound Healing

<130> 012679-093

<140> US 10/623,567
<141> 2003-07-22

<150> KR 10-2002-42858
<151> 2002-07-22

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 312
<212> PRT
<213> Homo sapiens

<400> 1
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            20              25                  30
Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu
        35                  40                  45
Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln
    50                  55                  60
Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe
65                  70                  75                  80
Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val
                85                  90                  95
Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln
            100                 105                 110
Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu
        115                 120                 125
Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
    130                 135                 140
Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly
145                 150                 155                 160
Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val
                165                 170                 175
Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly
            180                 185                 190
Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile
            195                 200                 205
Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln
        210                 215                 220
Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala
225                 230                 235                 240
Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe
                245                 250                 255
Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu
            260                 265                 270
```

Page 1

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Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
        275                 280                 285
Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
        290                 295                 300
Thr Met Ser Asn Ser Gly Ile Lys
305                 310
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<210> 2
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> probe for Southern blot

<400> 2
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gcgcagctgt gctcgacgtt gtcactgaag cgggaaggac tggctgct           108


<210> 3
<211> 1226
<212> DNA
<213> Artificial Sequence

<220>
<223> probe for Southern blot

<221> misc_feature
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68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 646, 647,
648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659,
660, 661, 662, 663, 1212, 1213, 1214, 1215, 1216, 1217
<223> n = A,T,C or G

<221> misc_feature
<222> 1218, 1219, 1220, 1221
<223> n = A,T,C or G

<400> 3
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nnnnnnnnnn nnnnnnnnng aattcaataa ggagactttt taaaaagata tttttatctt 120
aatgtgtgtg tgcctgcatt tgtgtgtatg caccattgcg tgcataccta gagcctgcag 180
aggctagaag aggggttcaa cctggaactg aggctacagg tggttgttga gtatccacat 240
agatgctcgg aattaaacct gggttctcca gtcccaagga gactaaatat tttcaaagta 300
agcctgcact ttgtactaca gtaaaataaa accactgtgg agtgactaat ataaaatagt 360
aagatgagct ctagattaac aggcaaaagt ttaagttttc agtattgtta aagtagcacc 420
atctccctaa agagaaccat atttattttc cttccagtct tctgtgtttc cctcttttgt 480
ttgaaagttt agtgagtgct tattttctct actgtgaaca caacatgaga caaactcagg 540
gattgtaaga gatcatggac ataaattact tttaggaacc tggcactcaa atgaaaatta 600
attagtgaca agttggcatg gcattttatt attaaccctg ggtggnnnnn nnnnnnnnnn 660
nnntaaactg cgtggtgatg atttgtgatt gcaagaagac atagatatga agctctgaac 720
aacagtgtcc aggcaacatg tgaagaaaag gccctatgga ggggcaggag agcaggtgag 780
agcatcctaa tagaaattca gacagtgaag caagaagttg ttcacacagc ccacacagcc 840
tgttaagtgt tcttcactta aggtttgttg actgtaacca ccttttctaa agaaaacatt 900
aagaaaaaca taggtgtctg ttcgcttcct atttgctgct gtgattaaaa cgctgaccaa 960
aagcaacttg gctgaggagc cgtttttgta tttctccgtt taggtagcaa tgaagttgga 1020
gcaggaggaa gggtgcttac aggctagctc tcctgctctc cttgagcaag cattcttgtg 1080
gtagctcagg actccctgca cagtgacaca ccacgtgctt cttcaggggg acttcaaact 1140
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gcttgagtat tnnnnnnnnn nagctt                                       1226
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<212> DNA
<213> Artificial Sequence

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<223> IF3 primer for PCR

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<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> IR3 primer for PCR

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<210> 6
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> pKOF2 primer for PCR

<400> 6
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<210> 7
<211> 838
<212> DNA
<213> Artificial Sequence

<220>
<223> p43-specific probe for Northern blot

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ctgaagaggc tggagcagaa gggtgcagag gcggatcaga tcatcgaata tctcaagcag 120
caggttgctc ttcttaagga gaaagcaatt ttgcaggcaa caatgagaga agaaaagaaa 180
cttcgagttg aaaatgctaa actgaaagaa gaaatagaag agctaaagca agagctgatt 240
ctggcagaaa ttcataacgg agtggagcaa gtgcgtgttc gattgagtac tccactgcag 300
acgaactgta ctgcttctga agtgtggtg cagtctccat cagtagcaac caccgcctct 360
cctgctacaa aagagcagat caaagcggga gaagaaaaga aggtgaaaga gaagactgaa 420
aagaaaggag agaaaaagga gaagcagcag tcggcagcag caagtactga ctccaagcct 480
atcgacgcat cgcgtctgga tcttcgaatt ggttgtattg ttactgccaa gaagcaccct 540
gatgcagatt cactgtatgt ggaggaagta gatgtgggag aagcagcccc gcgcacggtc 600
gtcagcgggc tggtgaatca tgttcctcta gaacagatgc aaaatcgtat ggtggttta 660
ctctgtaatc tgaagcctgc aaagatgcgg ggagttctgt ctcaagccat ggtgatgtgt 720
gccagttcac cagagaaagt ggagattctg ccccctccca cgggtccgt tcctggggac 780
agaattactt ttgatgcttt tcctggagag cctgacaagg agctaaaccc taagaaga    838
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